

In this issue

Editorial — Goodbye to CFG

Sadly, this will be the last issue of *Comparative and Functional Genomics*. Our Editor-in-Chief, **Stephen Oliver**, thanks all those who were involved in publishing the journal.

In silico analysis for transcription factors with Zn(II)₂C₆ binuclear cluster DNA binding domains in *Candida albicans*

6047 *C. albicans* open reading frames were screened for Zn(II)₂C₆-type zinc cluster domains (or binuclear cluster domains) involved in DNA recognition, by **Sergi Maicas** *et al.* These fungal transcription regulators control genes involved in a wide range of cellular processes including metabolism of different compounds such as sugars or amino acids, multi-drug resistance, control of meiosis, cell wall architecture, etc. The selection criteria used in the sequence analysis were the presence of the CysX₂CysX₆CysX_{5–16}CysX₂CysX_{6–8} Cys motif and a putative nuclear localization signal. Using this approach, 70 putative Zn(II)₂C₆ transcription factors were found in the genome of *C. albicans*.

Meeting Review — eGenomics: genomes and the environment

Environmental genomics is the investigation of how living organisms adapt to and are impacted by their environments using genomic technologies. **Dawn Field and colleagues** report from a workshop held on September 5th to 6th 2005, which aimed to examine current work at the interface between genomes and environmental science and to explore future prospects for the development of this important interface.

Meeting Review — eGenomics: Cataloguing our Complete Genome Collection

There is increasing recognition that the scientific community would benefit from the development of a new standard to capture a richer set of information describing complete genomes. **Dawn Field and colleagues** report from a Workshop held on September 7th to 9th 2005 with the aim of addressing this need.

Special section of papers from the Bio-Ontologies special interest group meeting at ISMB 2005

Robert Stevens and co-organisers open this special section with a report from the 8th Annual Bio-Ontologies special interest group meeting.

Mary Shimoyama and colleagues describe how the Rat Genome Database has developed a comprehensive ontology-based data structure and annotation system to integrate physiological data with environmental and experimental factors, and genetic and genomic information.

Barry Smith *et al.* present an extension of their approach (in which the provision of formal definitions for relations such as *is_a*, *part_of* and *transformation_of* can facilitate the integration of biomedical ontologies) to the treatment of pathologies, focusing especially on those pathological continuant entities that arise when organs become affected by carcinomas.

Pankaj Jaiswal and colleagues describe the Plant Ontology, a collaborative effort among several plant databases and experts in plant systematics, botany and genomics, and give us a detailed update on the current version, which integrates diverse vocabularies used to describe anatomy, morphology and growth stages of *Arabidopsis*, maize and rice.

Daniel McShan discusses the state of the art in biochemical databases and how these sources may be applied to the problem of classifying compounds based solely on structure. He describes a biochemical informatics system for processing molecular data and describes how 100,255 compositional (hasA) relationships are inferred between 835 abstractions and 9500 metabolites from the KEGG Ligand database.

Conference calendar

A listing of genomics related conferences planned for March to May 2006.

Thank you to reviewers

We take the opportunity to thank all our external reviewers of papers for CFG.